

REMARKS

Claims 31-60 are all the claims presently pending in the application.

It is noted that the claim amendments herein or later are not made to distinguish the invention over the prior art or narrow the claims or for any statutory requirements of patentability. Further, Applicant specifically states that no amendment to any claim herein or later should be construed as a disclaimer of any interest in or right to an equivalent of any element or feature of the amended claim.

Claim 53 stands rejected under 35 USC §101 as being allegedly directed to non-statutory subject matter.

Claims 31-60 stand rejected under 35 USC §103(a) as being allegedly unpatentable over Ishikawa et al. ("FramePlot: a new implementation of the Frame analysis for predicting protein-coding regions in bacterial DNA with a high G + C content", FEMS Microbiology Letters 174 (1999) 251-253) (hereinafter "Ishikawa"), in view of Floratos et al. ("Sequence Homology Detection Through Large Scale Pattern Discovery" (1999) (hereinafter "Floratos").

These rejections are respectfully traversed in the following remarks

I. THE CLAIMED INVENTION

The claimed invention (e.g., as recited in claim 1) is directed to a system for identifying genes. The system includes a pattern database comprising patterns of amino acids, and an input device for inputting a genomic DNA sequence. The system further includes a processor which translates an open reading frame (ORF) of the DNA sequence into an amino acid translation.

Importantly, the processor locates in the amino acid translation occurrences of the patterns from the pattern database, and determines whether the open reading frame includes a putative gene based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns of amino acids located in the amino acid translation of the ORF (Application at page 13, lines 2-19).

Conventional systems for identifying genes (e.g., putative genes) are either based on the use the statistics of DNA sequences, or the use of similarity searches to determine gene

locations (Application at page 2, lines 7-22). However, these conventional methods have various problems which prevent them from efficiently identifying genes in a given DNA sequence (Application at page 3, line 19-page 4, line 21).

The claimed invention, on the other hand, includes a processor which **locates in the amino acid translation occurrences of the patterns from the pattern database, and determines whether the open reading frame includes a putative gene based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns** of amino acids located in the amino acid translation of the ORF (Application at page 13, lines 2-19). The claimed invention may be considered as including the best characteristics of statistical approaches and database similarity searches, in identifying genes in a given DNA sequence (Application at page 6, lines 18-21).

II. THE 35 USC §101 REJECTION

The Examiner surprisingly alleges that claim 53 is directed to non-patentable subject matter. Applicant respectfully submits that the Examiner is incorrect.

In particular, the Examiner alleges on page 3 of the Office Action that "applicant has provided evidence that applicant intends the 'medium' to include transmission signals".

However, Applicant would point out to the Examiner that the specification states that "the instructions may be **stored** on a variety of machine-readable data **storage media**" (Application at page 22, lines 18-19; emphasis added).

Moreover, Applicant would point out that the claim recites "[a] programmable storage medium **tangibly embodying** a program of machine-readable instructions". Applicant respectfully submits that a "transmission signal" is **inherently intangible** and could not **tangibly** embody a program as asserted by the Examiner. That is, it is completely unreasonable for the Examiner to construe claim 53 to cover instructions included merely in a transmission signal.

Thus, the Examiner's assertions are completely unreasonable.

In view of the foregoing, the Examiner is respectfully requested to withdraw this rejection.

III. THE ALLEGED PRIOR ART REFERENCES

The Examiner alleges that Ishikawa would have been combined with Floratos to form the invention of claims 31-60. Applicant submits, however, that Ishikawa would not have been combined with Floratos and even if combined, the combination would not teach or suggest each and every feature of the claimed invention.

Applicant respectfully submits that these references would not have been combined as alleged by the Examiner. Indeed, these references are unrelated, and no person of ordinary skill in the art would have considered combining these disparate references, absent impermissible hindsight.

In fact, these references clearly do not teach or suggest their combination. Therefore, Applicant respectfully submits that one of ordinary skill in the art would not have been so motivated to combine the references as alleged by the Examiner. Therefore, the Examiner has failed to make a prima facie case of obviousness.

In particular, Applicant would again point out that an exemplary aspect of the claimed invention (e.g., as recited, for example, in claim 1) includes a processor which **locates in the amino acid translation occurrences of the patterns from the pattern database, and determines whether the open reading frame includes a putative gene based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns of amino acids located in the amino acid translation of the ORF** (Application at page 13, lines 2-19). The exemplary aspects of the claimed invention may be considered as including the best characteristics of statistical approaches and database similarity searches, in identifying genes in a given DNA sequence (Application at page 6, lines 18-21).

Clearly, these features are not taught or suggested by the cited references.

Indeed, Ishikawa is unrelated to the claimed invention. Ishikawa discloses a web-based tool for predicting protein-coding regions in bacterial DNA. The tool outputs a "clickable map" which allows a user to click on an ORF to provide the nucleotide sequence and its deduced

amino acid sequence. The user can then compare these sequences with a sequence database over the Internet, for example, by searching the NCBI BLAST server (Ishikawa at Abstract; Figure 1).

However, even assuming (arguendo) that Ishikawa teaches plotting a putative ORF and generating a deduced amino acid sequence by clicking on the ORF, nowhere does Ishikawa teach or suggest a pattern database, as in the claimed invention. In fact, the Examiner expressly concedes this on page 4 of the Office Action. Therefore, Ishikawa certainly does not teach or suggest a processor which **locates in the amino acid translation occurrences of the patterns from the pattern database, and determines whether the open reading frame includes a putative gene based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns of amino acids located in the amino acid translation of the ORF.**

The Examiner alleges that Floratos makes up for the deficiencies of Ishikawa. This is clearly incorrect.

Indeed, Applicant would AGAIN point out that Floratos is unrelated to the claimed invention. In fact, Floratos simply discloses using patterns to perform similarity searching between a query protein Q (i.e., a known protein) and a database of proteins (Floratos at Abstract; Section 3.1, page 165). That is, the object of Floratos is "the identification of homologies between a query sequence and the proteins of the data base at hand" (Floratos at Section 5, page 168).

In fact, the present Application acknowledges Floratos on pages 10-11, stating that "[t]he availability of such a collection of patterns permits a user to effectively and successfully tackle a number of tasks including, for example, similarity searching (e.g., see Floratos, A., Rigoutsos, I., et al., (1999) "Sequence Homology Detection Through Large Scale Pattern Discovery", *Proc. RECOMB '99*)". Thus, it is completely unreasonable to rely on Floratos as teaching anything more than similarity searching.

In fact, the Examiner surprisingly alleges that Floratos discloses many features which Floratos most certainly does not. Indeed, Applicant would respectfully submit that the Examiner mischaracterizes Floratos.

First, on page 5 of the Office Action, the Examiner alleges that "Floratos describes: ... d. Locates in said **amino acid translation** occurrences of said patterns from said pattern database (page 165, column 2, Pattern Matching section)" (emphasis added). This is certainly not correct. Indeed, as noted above, Floratos simply teaches identifying similarities between a query protein Q (i.e., a known protein) and a database of proteins. However, the amino acid translation of the claimed invention is translated from an open reading frame (ORF) of a DNA sequence. Applicant would remind the Examiner that an open reading frame (ORF) may be defined as a portion of a genome which contains a sequence of bases that could potentially encode for a protein. **Since Floratos's query sequence is a known protein, Floratos would have no use for an amino acid translation of an ORF.**

Moreover, **it is completely unreasonable for the Examiner to suggest that Ishikawa would have been combined with Floratos.**

Second, the Examiner alleges on page 5 of the Office Action that Floratos "[d]etermines whether said open reading frame includes a putative gene based on a number of said patterns of amino acids located in said amino acid translation of said ORF (page 167, column 2, section 4.1)". This too is clearly incorrect.

Indeed, as noted above, Floratos does not teach or suggest anything about an open reading frame (ORF) or an "amino acid translation" of an ORF. The Examiner is mischaracterizing Floratos in a desperate attempt to reject the claims of the present Application.

In fact, Section 4.1 on page 167 of Floratos discloses simply "Information Gathering" which involves simply gathering significant patterns (e.g., see Section 2, column 1 on page 165; and Section 3.2 on pages 166, 167).

Thus, nowhere in this passage, or anywhere else for that matter, does Floratos teach or suggest a processor which **determines whether an open reading frame includes a putative gene based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns of amino acids located in the amino acid translation of the ORF.**

Therefore, Floratos clearly does not make up for the deficiencies of Ishikawa.

Therefore, Applicant submits that these alleged references would not have been combined and even if combined, the combination would not teach or suggest each and every element of the claimed invention. Therefore, the Examiner is respectfully requested to withdraw this rejection.


IV. FORMAL MATTERS AND CONCLUSION

In view of the foregoing, Applicant submits that claims 31-60, all the claims presently pending in the application, are patentably distinct over the prior art of record and are in condition for allowance. The Examiner is respectfully requested to pass the above application to issue at the earliest possible time.

Should the Examiner find the application to be other than in condition for allowance, the Examiner is requested to contact the undersigned at the local telephone number listed below to discuss any other changes deemed necessary in a telephonic or personal interview.

The Commissioner is hereby authorized to charge any deficiency in fees or to credit any overpayment in fees to Assignee's Deposit Account No. 50-0510.

Respectfully Submitted,



Date: August 7, 2008

Phillip E. Miller, Esq.
Registration No. 46,060

McGinn IP Law Group, PLLC
8321 Old Courthouse Road, Suite 200
Vienna, VA 22182-3817
(703) 761-4100
Customer No. 48150